

Seq1: Hi-AF (104 mers)

5'-gatacctttatggttggttacactgactgactgaatccggtcagaaacctgtgcctgtg  
cgaaggetctaacgthgcccagggcaacaatgcatcctgggc-3'

Seq2: Hi-AR (107 mers)

5'-ctctagagcccaggatgcatttggtgccctggccgcaaacgtagagccttcgcacag  
gcacagggtctgaccggattcagtgagtcagtgtaadacaaccataaag-3'

Seq3: Hi-BF (111 mers)

5'-tctagaggcgaaaaaataatgcgttactggcggaaggtagctccacaaggcttgaat  
cccgggaagaatagaaaccgcagtcctccgacgacagaacctgcaataatagggc-3'

Seq4: Hi-BF (108 mers)

5'-ggccgccctattatgcagggtattcttcagggtattcttcaagtcgccgtcgttgtg  
agactgcggthtcggagtagcttcgccagtaacgcattgattttttcgc-3'

Figure 1

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Seq5: Hi-PCR-AF (33 mers)  
5'-tcgggatcctttatggttgtttacactgactgc-3'

Seq6: Hi-PCR-AR (31 mers)  
5'-gcctctagagcccaggatgcatttgttggcc-3'

Seq7: Hi-PCR-BF (38 mers)  
5'-ggctctagaggcgaaaaaatcaatgcgttactggcga-3'

Seq8: Hi-PCR-BR (32 mers)  
5'-catgcggccgccctattattgcaggtattctt-3'

Figure 2

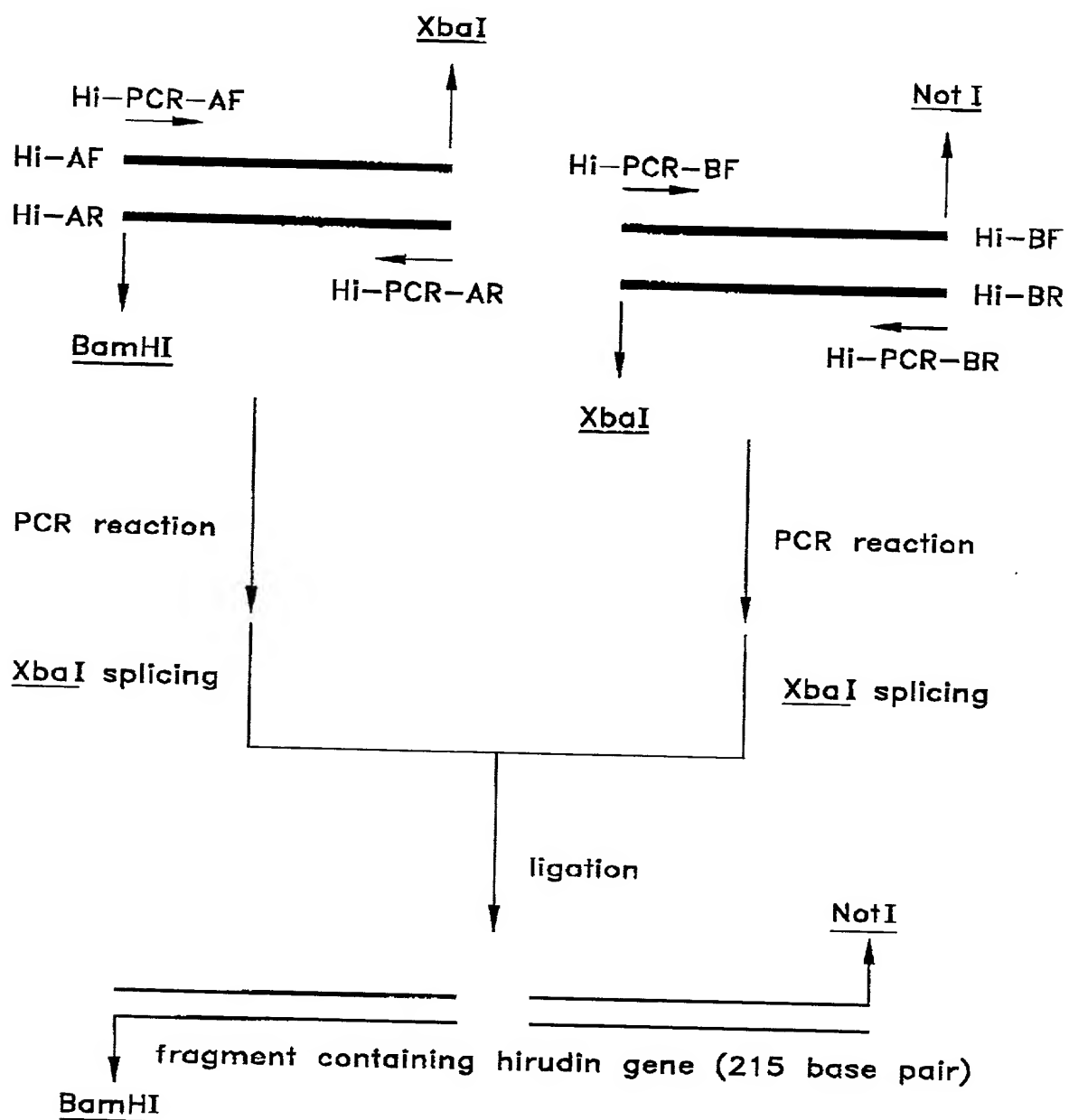


Figure 3

(A)

GATCCTTT ATG GTT GTT TAC ACT GAC TGC ACT GAA TCC GGT CAG  
AAC CTG TGC CTG TGC GAA GGC TCT AAC GTT TGC GGC CAG GGC  
AAC AAA TGC ATC CTG GGC TCT AGA GGC GAA AAA AAC CAG TGC  
GTT ACT GGC GAA GGT ACC CCG AAA CCG CAG TCT CAC AAC GAC  
GGC GAC TTC GAA GAA ATC CCG GAA GAA TAC CTG CAG TAA TAGGGC

(B)

Met Val Val Tyr Thr Asp Cys Thr Glu Ser Gly Gln Asn Leu  
Cys Leu Cys Glu Gly Ser Asn Val Cys Gly Gln Gly Asn Lys  
Cys Ile Leu Gly Ser Arg Gly Glu Lys Asn Gln Cys Val Thr  
Gly Glu Gly Thr Pro Lys Pro Gln Ser His Asn Asp Gly Asp  
Phe Glu Glu Ile Pro Glu Glu Tyr Leu Gln

Figure 4

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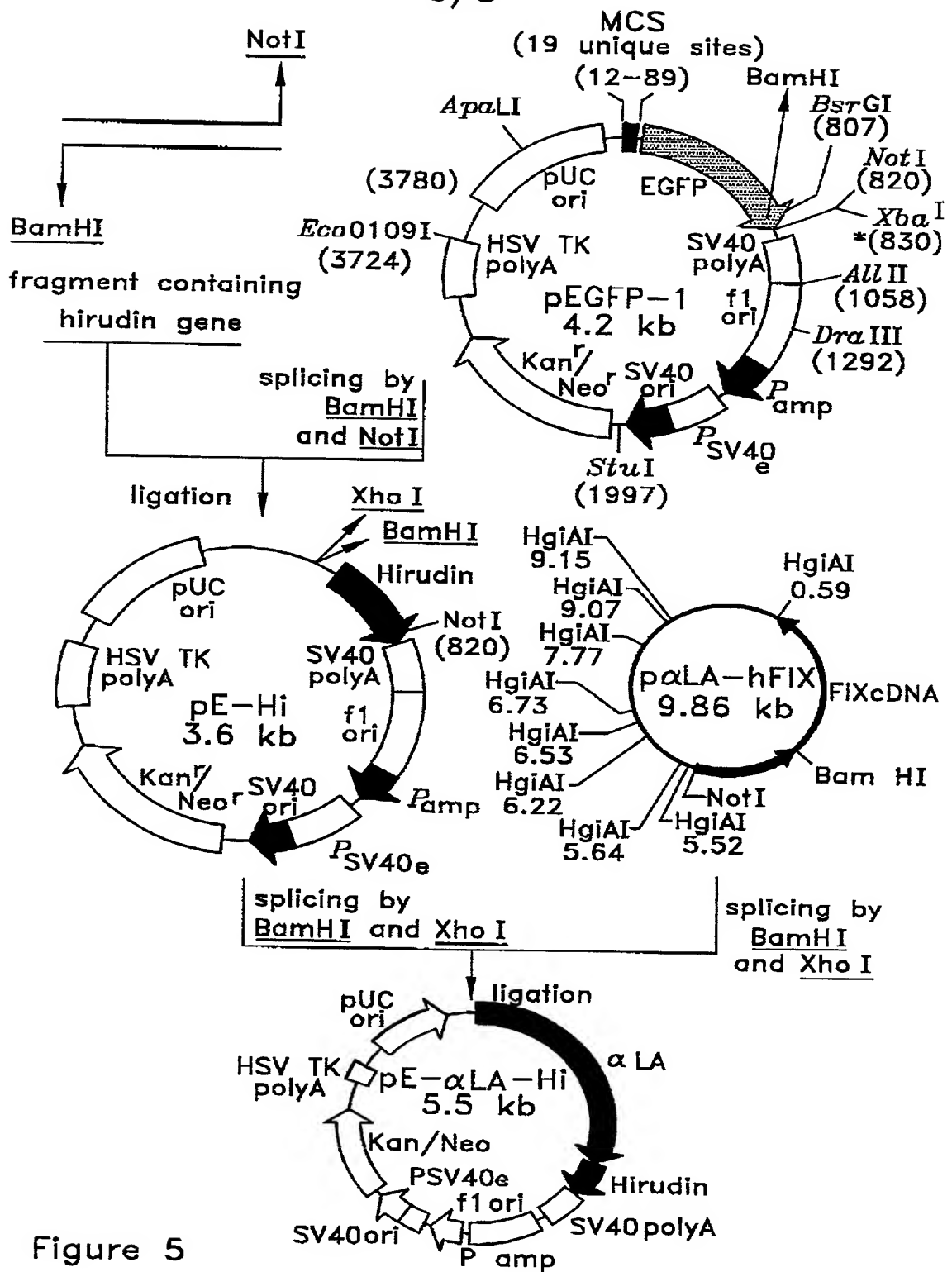


Figure 5

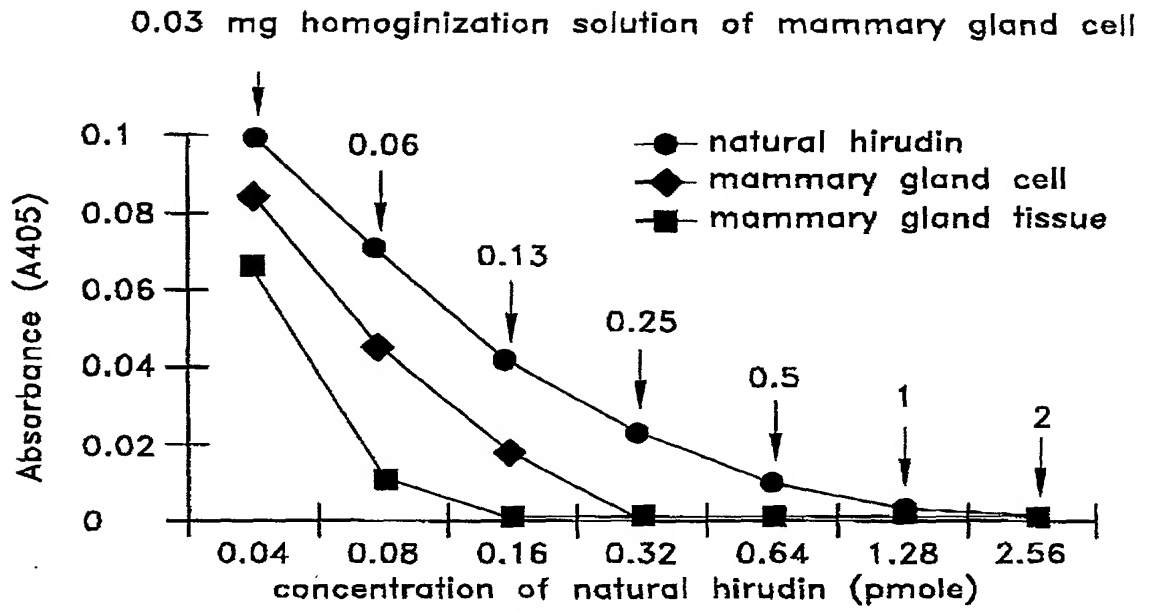


Figure 6

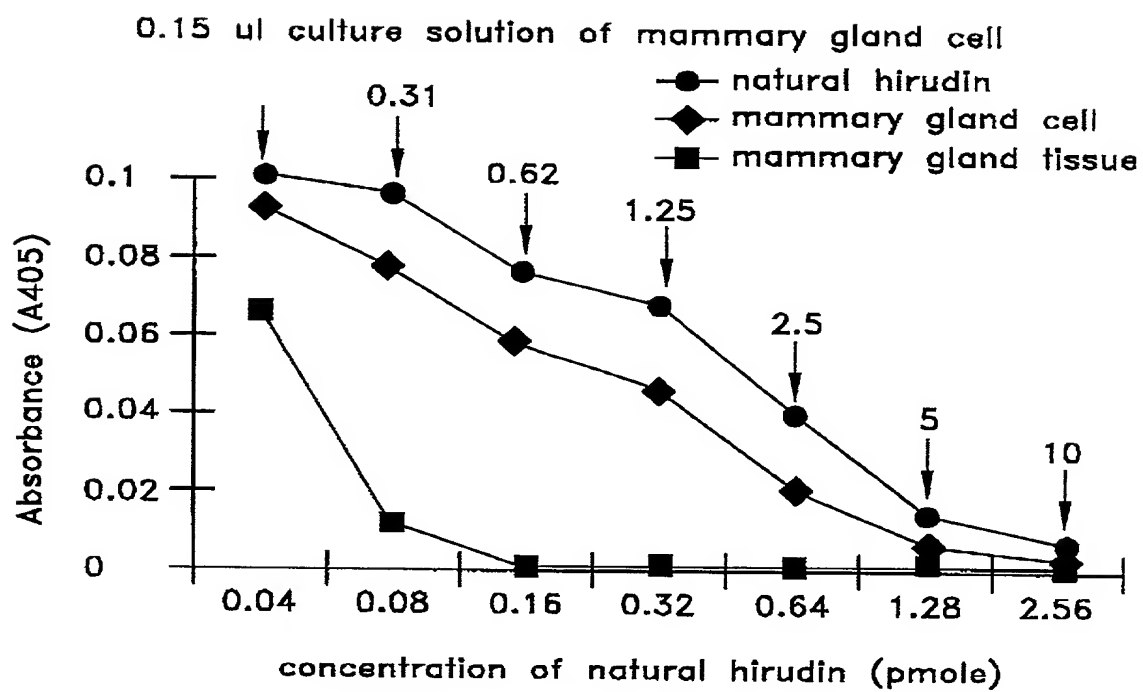


Figure 7

**Fig. 8**